2002-011 seq 1st
SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> novel Brachyspira hyodysenteriae vaccine

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<170> PatentIn version 3.1

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<211> 1614

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<213> Brachyspira hyodysenteria

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<221> CDS

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1               5                   10                  15

att tat tca tgc gga agt tat ttt aat cct aaa tac tat ttt ttt aaa        96
Ile Tyr Ser Cys Gly Ser Tyr Phe Asn Pro Lys Tyr Tyr Phe Phe Lys
                20                  25                  30

agt aaa gta gag aat aat gga agt tct gga agc tca ggc ggt aat tca       144
Ser Lys Val Glu Asn Asn Gly Ser Ser Gly Ser Ser Gly Gly Asn Ser
            35                  40                  45

gga ata tat ata cag cct ggt gaa gat gaa gat cct ttt aca gca cct       192
Gly Ile Tyr Ile Gln Pro Gly Glu Asp Glu Asp Pro Phe Thr Ala Pro
        50                  55                  60

aaa tat gca tct gag tgg tgg aat gat cct aat aat ggt gga ttt gat       240
Lys Tyr Ala Ser Glu Trp Trp Asn Asp Pro Asn Asn Gly Gly Phe Asp
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65   70   75   80

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gct tcg gat ata gat aaa tgg ttt ttg aaa gtt gaa ttt tta gca aat      288
Ala Ser Asp Ile Asp Lys Trp Phe Leu Lys Val Glu Phe Leu Ala Asn
            85                  90                  95

gat tat cca agt tac aga ttt tta aca aaa agc gga aga aaa gca gga      336
Asp Tyr Pro Ser Tyr Arg Phe Leu Thr Lys Ser Gly Arg Lys Ala Gly
            100                 105                 110

cat gtt tgg gta gtt tct aat gaa caa tct cag gca tat tta gat caa      384
His Val Trp Val Val Ser Asn Glu Gln Ser Gln Ala Tyr Leu Asp Gln
            115                 120                 125

gga gaa gta tgc aat act aca gca gtt acc ggg gta tct ata aaa cca      432
Gly Glu Val Cys Asn Thr Thr Ala Val Thr Gly Val Ser Ile Lys Pro
            130                 135                 140

gta gca aat gta aca gga gta aca tat aca aaa tat aag gga ttg aat      480
Val Ala Asn Val Thr Gly Val Thr Tyr Thr Lys Tyr Lys Gly Leu Asn
145                 150                 155                 160

gca aga ttt ttc act cat gac gga gat tat cat aat gta tat cct gga      528
Ala Arg Phe Phe Thr His Asp Gly Asp Tyr His Asn Val Tyr Pro Gly
            165                 170                 175

aaa gat aag ata agc aga ttc tat ttt tat tat ttt aca ggt act ccg      576
Lys Asp Lys Ile Ser Arg Phe Tyr Phe Tyr Tyr Phe Thr Gly Thr Pro
            180                 185                 190

gaa atg gct aaa ttt tta gaa aat tgc tta ata gct gta gac aca tac      624
Glu Met Ala Lys Phe Leu Glu Asn Cys Leu Ile Ala Val Asp Thr Tyr
            195                 200                 205

tca aaa cta tta ttt tac tat gga aga cct caa agc gat tat cca aat      672
Ser Lys Leu Leu Phe Tyr Tyr Gly Arg Pro Gln Ser Asp Tyr Pro Asn
            210                 215                 220

cct cca agc tgg cag aag cct agt aat ttg gtt gat aaa tac tct cct      720
Pro Pro Ser Trp Gln Lys Pro Ser Asn Leu Val Asp Lys Tyr Ser Pro
225                 230                 235                 240

aca ggt tat tgg ata tct ata gat gaa ggt ata aat gat aag ggg cag      768
Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
            245                 250                 255

aat tat cct ttt tat gaa tat gat cct gta gga tat gta aaa agc gat      816
Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
            260                 265                 270

ggt aca gtt gtt ata ttt gat tgg ttt gca aac aga tta aga gga aat      864
Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
            275                 280                 285

cat aat aat gat cct ata aaa agt gat cct aaa gga gct att gtt cct      912
His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
            290                 295                 300

aat cct aat act aat cct tct gct tca act aca gga cgt tct cct tat      960
Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
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gca ttc tat tcg cct tta gca caa aaa gat aaa act aaa ata act ata     1008
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Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
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agt act aca aaa tta ata aat tat aca gtt ttc agt tat aaa tac agt        1056
Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
            340             345             350

ata caa ata ttt ccg cct agt atg aaa gaa gaa aaa ctt cct tat gct        1104
Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
            355             360             365

tat att gca tat gct tcc tat ggt gca gct tat caa aat gaa agc agc        1152
Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
            370             375             380

aaa tct gta gag atg ata tct gat ata aat aaa gga gag cat tac gga        1200
Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385             390             395             400

agt att aca aga ata agc act gta cct aaa ata gat aaa gac gga gga        1248
Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
            405             410             415

gag ttg gta aaa gaa gga tct aag tct ttt gaa tta tat ggt att gat        1296
Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
            420             425             430

act aaa gat aca ttt ata gaa tta agt tta aaa cta att aaa aat gat        1344
Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
            435             440             445

gaa aat aca gaa ttt gtt gat caa gga aca gca ggt act ggt cct tta        1392
Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
            450             455             460

gta tac ttt gat aaa aca gat cct ata ctt gta tta aaa tat gat aaa        1440
Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465             470             475             480

tct tct gac agc ttc aaa tac agc agt gta aaa gga aac aag caa ata        1488
Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile
            485             490             495

gaa gtt gac agc aat tta tca att aaa aga gga gag aat aaa gag ttt        1536
Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
            500             505             510

aca gtt aaa ttt aaa gat cca aat aat gga aat gag ttt ggg gtt gta        1584
Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
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ttt aaa ata gat ttt gaa aaa ata tca tga                                1614
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<213> Brachyspira hyodysenteria

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Ser	Lys	Val	Glu	Asn	Asn	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Gly	Asn	Ser
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Gly	Ile	Tyr	Ile	Gln	Pro	Gly	Glu	Asp	Glu	Asp	Pro	Phe	Thr	Ala	Pro
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Lys	Tyr	Ala	Ser	Glu	Trp	Trp	Asn	Asp	Pro	Asn	Asn	Gly	Gly	Phe	Asp
65					70					75					80

Ala	Ser	Asp	Ile	Asp	Lys	Trp	Phe	Leu	Lys	Val	Glu	Phe	Leu	Ala	Asn
				85					90					95	

Asp	Tyr	Pro	Ser	Tyr	Arg	Phe	Leu	Thr	Lys	Ser	Gly	Arg	Lys	Ala	Gly
			100					105					110		

His	Val	Trp	Val	Val	Ser	Asn	Glu	Gln	Ser	Gln	Ala	Tyr	Leu	Asp	Gln
		115					120					125			

Gly	Glu	Val	Cys	Asn	Thr	Thr	Ala	Val	Thr	Gly	Val	Ser	Ile	Lys	Pro
	130					135					140				

Val	Ala	Asn	Val	Thr	Gly	Val	Thr	Tyr	Thr	Lys	Tyr	Lys	Gly	Leu	Asn
145					150					155					160

Ala	Arg	Phe	Phe	Thr	His	Asp	Gly	Asp	Tyr	His	Asn	Val	Tyr	Pro	Gly
				165					170					175	

Lys	Asp	Lys	Ile	Ser	Arg	Phe	Tyr	Phe	Tyr	Tyr	Phe	Thr	Gly	Thr	Pro
			180					185					190		

Glu	Met	Ala	Lys	Phe	Leu	Glu	Asn	Cys	Leu	Ile	Ala	Val	Asp	Thr	Tyr
	195					200					205				

Ser	Lys	Leu	Leu	Phe	Tyr	Tyr	Gly	Arg	Pro	Gln	Ser	Asp	Tyr	Pro	Asn
	210				215					220					

Pro	Pro	Ser	Trp	Gln	Lys	Pro	Ser	Asn	Leu	Val	Asp	Lys	Tyr	Ser	Pro
225					230					235					240

Thr Gly Tyr Trp Ile Ser Ile Asp Glu Gly Ile Asn Asp Lys Gly Gln
            245   250   255

Asn Tyr Pro Phe Tyr Glu Tyr Asp Pro Val Gly Tyr Val Lys Ser Asp
            260   265   270

Gly Thr Val Val Ile Phe Asp Trp Phe Ala Asn Arg Leu Arg Gly Asn
            275   280   285

His Asn Asn Asp Pro Ile Lys Ser Asp Pro Lys Gly Ala Ile Val Pro
290   295   300

Asn Pro Asn Thr Asn Pro Ser Ala Ser Thr Thr Gly Arg Ser Pro Tyr
305   310   315   320

Ala Phe Tyr Ser Pro Leu Ala Gln Lys Asp Lys Thr Lys Ile Thr Ile
            325   330   335

Ser Thr Thr Lys Leu Ile Asn Tyr Thr Val Phe Ser Tyr Lys Tyr Ser
            340   345   350

Ile Gln Ile Phe Pro Pro Ser Met Lys Glu Glu Lys Leu Pro Tyr Ala
            355   360   365

Tyr Ile Ala Tyr Ala Ser Tyr Gly Ala Ala Tyr Gln Asn Glu Ser Ser
    370   375   380

Lys Ser Val Glu Met Ile Ser Asp Ile Asn Lys Gly Glu His Tyr Gly
385   390   395   400

Ser Ile Thr Arg Ile Ser Thr Val Pro Lys Ile Asp Lys Asp Gly Gly
            405   410   415

Glu Leu Val Lys Glu Gly Ser Lys Ser Phe Glu Leu Tyr Gly Ile Asp
            420   425   430

Thr Lys Asp Thr Phe Ile Glu Leu Ser Leu Lys Leu Ile Lys Asn Asp
        435   440   445

Glu Asn Thr Glu Phe Val Asp Gln Gly Thr Ala Gly Thr Gly Pro Leu
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Val Tyr Phe Asp Lys Thr Asp Pro Ile Leu Val Leu Lys Tyr Asp Lys
465   470   475   480

Ser Ser Asp Ser Phe Lys Tyr Ser Ser Val Lys Gly Asn Lys Gln Ile

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                485   490   495

Glu Val Asp Ser Asn Leu Ser Ile Lys Arg Gly Glu Asn Lys Glu Phe
            500   505   510

Thr Val Lys Phe Lys Asp Pro Asn Asn Gly Asn Glu Phe Gly Val Val
        515   520   525

Phe Lys Ile Asp Phe Glu Lys Ile Ser
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<213> Brachyspira hyodysenteria

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1   5   10   15

gga tgt gaa act atg cag cct aaa aat aat gat aca att gta aaa aat   96
Gly Cys Glu Thr Met Gln Pro Lys Asn Asn Asp Thr Ile Val Lys Asn
                20   25   30

gat aat tca tct aat gaa gat aaa aaa gaa gaa act ata act aga gaa   144
Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
            35   40   45

gat aca cca aaa atg aaa gtt aca gtt tat gga gca gat aaa gaa att   192
Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
    50   55   60

caa gct gtg gaa ata aat gat aaa act tat tat gta ata ggc gga aaa   240
Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65   70   75   80

gat gtt gag aat atg aca gaa gct gat ata aaa aaa tca tct tta gta   288
Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
                85   90   95

gca cct tta aaa gtt aca gaa gaa act gtt aat ggt aca aga ggt ata   336
Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
            100   105   110
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gtt gtt aca tat tat gat gta aaa gta ttc ttg ggt aaa aga aca gga          384
Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
        115             120             125

aca gga act atc gta gga ata ttc gag cct cag aaa aat gat tgg act          432
Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
    130             135             140

aca gga aat gat ttg gat aga agt tta tct att caa ata aaa tta tct          480
Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145             150             155             160

aga aat ata gca ggt cct ata gat ata aaa aga gga agc ata tct tta          528
Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
            165             170             175

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Ala Phe Asn
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<213> Brachyspira hyodysenteria

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Asp Asn Ser Ser Asn Glu Asp Lys Lys Glu Glu Thr Ile Thr Arg Glu
            35              40              45

Asp Thr Pro Lys Met Lys Val Thr Val Tyr Gly Ala Asp Lys Glu Ile
    50              55              60

Gln Ala Val Glu Ile Asn Asp Lys Thr Tyr Tyr Val Ile Gly Gly Lys
65              70              75              80

Asp Val Glu Asn Met Thr Glu Ala Asp Ile Lys Lys Ser Ser Leu Val
            85              90              95

Ala Pro Leu Lys Val Thr Glu Glu Thr Val Asn Gly Thr Arg Gly Ile
            100             105             110

Val Val Thr Tyr Tyr Asp Val Lys Val Phe Leu Gly Lys Arg Thr Gly
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               115   120   125

Thr Gly Thr Ile Val Gly Ile Phe Glu Pro Gln Lys Asn Asp Trp Thr
    130   135   140

Thr Gly Asn Asp Leu Asp Arg Ser Leu Ser Ile Gln Ile Lys Leu Ser
145   150   155   160

Arg Asn Ile Ala Gly Pro Ile Asp Ile Lys Arg Gly Ser Ile Ser Leu
                165   170   175

Ala Phe Asn